

## SEQUENCE LISTING

<110> M&E Biotech A/S  
 HALKIER, Torben  
 HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand  
 Activity

<130> 22021 PC 1

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tgc 229  
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser  
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gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277  
 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His  
 20 25 30

gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325  
 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser  
 35 40 45

atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373  
 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 50 55 60

gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata	421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75	
tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa	469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu	
80 85 90 95	
aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta	517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu	
100 105 110	
ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg	565
Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val	
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Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu	
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Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys	
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Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg	
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Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile	
195 200 205	
gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga	853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg	
210 215 220	
cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg	901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met	
225 230 235	
gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg	949
Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu	
240 245 250 255	
atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat	997
Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His	
260 265 270	

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 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu  
 275 280 285  
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 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln  
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 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 305 310 315  
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&lt;210&gt; 2

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
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Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
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Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
      65           70           75           80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
      85           90           95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
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Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
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Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
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Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
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Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
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Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
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Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
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Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      210          215          220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
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Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
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Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe

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Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro	
20 25 30	
gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc	144
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser	
35 40 45	
atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc	192
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	
50 55 60	
atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata	240
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75 80	

tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa	288
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu	
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Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro	
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gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag	384
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys	
115 120 125	
gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct	432
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala	
130 135 140	
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165 170 175	
ggg tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg	576
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp	
180 185 190	
gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac	624
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn	
195 200 205	
caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat	672
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His	
210 215 220	
gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat	720
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225 230 235 240	
gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa	768
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys	
245 250 255	
gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat	816
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr	
260 265 270	
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Ser Ile Asn Val Gly Gly Phe Lys Leu Arg Ala Gly Glu Glu Ile	
275 280 285	

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 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
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Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
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Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
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Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
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Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
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Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
 195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
 225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
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gggagagaac gatcgcgagg cagggcgccc gaactccggg cgccgcgcc atg cgc cgg 178  
 Met Arg Arg

1

gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc 226  
 Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly  
 5 10 15

agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct 274  
 Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser  
 20 25 30 35

gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg 322  
 Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu  
 40 45 50



gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg	370
Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu	
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ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata tca gaa gac	418
Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp	
70 75 80	
agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt	466
Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly	
85 90 95	
ttg cag gac tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc	514
Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys	
100 105 110 115	
agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa	562
Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln	
120 125 130	
cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa	610
His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu	
135 140 145	
ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca	658
Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro	
150 155 160	
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165 170 175	
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Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile	
180 185 190 195	
tct aac atg acg tta agc aac gga aaa cta agg gtt aac caa gat ggc	802
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly	
200 205 210	
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Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser	
215 220 225	
gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa	898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys	
230 235 240	
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc	946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser	
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10

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gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag 1042
Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln
                280                285                290

gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt 1090
Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe
                295                300                305

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Gly Ala Phe Lys Val Gln Asp Ile Asp
                310                315

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taagactact aagagacatg gcccacggtg tatgaaactc acagccctct ctcttgagcc 1260

tgtacagggt gtgtatatgt aaagtcata ggtgatgtta gattcatggt gattacacaa 1320

cggttttaca attttgtaat gatttcctag aattgaacca gattgggaga ggtattccga 1380

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actgtttctg gtgaccacat gtagtttatt tctttattct ttttaactta atagagtctt 1860

cagacttgtc aaaactatgc aagcaaaata aataaataaa aataaaatga ataccttgaa 1920

taataagtag gatgttggtc accagggtgcc tttcaaattt agaagctaatt tgactttagg 1980

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gtgaaagtta ttttattata ctgtacaata aaagcattgt ctctgaatgt taattttttg 2220

gtacaaaaaa taaatttgta cgaaaacctg aaaaaaaaaa aaaaaaaggg cggccgctct 2280

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2299

&lt;210&gt; 6

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 6

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Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
 195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
 225 230 235 240

12

Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys
				245					250					255	

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Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
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Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
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<223> Description of Artificial Sequence: Synthetic PCR product with optimum codons for E. coli and P. pastoris expression

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<223> His tag

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<223> C-terminal part of *Saccharomyces cerevisiae*  
alpha-mating factor

$\langle 220 \rangle$

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<222> (85) . . (561)

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1 5 10 15

13

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cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt 144
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
                35                40                45

tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct 192
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
                50                55                60

aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag 240
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
                65                70                75                80

gac ggt ttp tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa 288
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
                85                90                95

acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt 336
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
                100                105                110

ggt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt 384
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
                115                120                125

ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct 432
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
                130                135                140

atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct 480
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
                145                150                155                160

atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc 528
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
                165                170                175

tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag 564
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                180                185

```

&lt;210&gt; 8

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Synthetic PCR  
product with optimum codons for E. coli and P.  
pastoris expression

14

&lt;400&gt; 8

Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys  
 1 5 10 15

His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala  
 20 25 30

Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly  
 35 40 45

Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala  
 50 55 60

Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln  
 65 70 75 80

Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu  
 85 90 95

Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val  
 100 105 110

Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly  
 115 120 125

Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser  
 130 135 140

Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser  
 145 150 155 160

Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr  
 165 170 175

Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

&lt;210&gt; 9

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: DNA encoding  
 murine OPGL, residues 158-316, fused to His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(519)

&lt;223&gt; Murine OPGL, residues 158-316

&lt;400&gt; 9

```

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1                      5                      10                      15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20                      25                      30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35                      40                      45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50                      55                      60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65                      70                      75                      80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85                      90                      95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100                      105                      110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115                      120                      125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
      130                      135                      140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
      145                      150                      155                      160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      165                      170

```

&lt;210&gt; 10

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: DNA encoding  
murine OPGL, residues 158-316, fused to His tag

&lt;400&gt; 10

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
165 170

&lt;210&gt; 11

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion of  
murine OPGL, residues 158-316 with C to S  
mutation, and His tag



<220>  
 <221> CDS  
 <222> (1)..(519)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(228)  
 <223> Murine OPGL, residues 158-219

<220>  
 <221> misc\_feature  
 <222> (232)..(519)  
 <223> Murine OPGL, residues 221-316

<220>  
 <221> mutation  
 <222> (229)..(231)  
 <223> tgt (Cys) to tcc (Ser)

<220>

<400> 11

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct	48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro	
1 5 10 15	
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct	96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
20 25 30	
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt	144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
35 40 45	
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt	192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
50 55 60	
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat	240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His	
65 70 75 80	
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt	288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	

18

```

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
      130              135              140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
      145              150              155              160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      165              170

```

&lt;210&gt; 12

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion of  
murine OPGL, residues 158-316 with C to S  
mutation, and His tag

&lt;400&gt; 12

```

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
  1              5              10              15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20              25              30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35              40              45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50              55              60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
      65              70              75              80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85              90              95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

```

19

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 165 170

&lt;210&gt; 13

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(564)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(336)

&lt;223&gt; Murine OPGL, residues 158-255

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (337)..(399)

&lt;223&gt; Tetanus toxoid P30 epitope

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (400)..(564)

&lt;223&gt; Murine OPGL, residues 262-316

&lt;400&gt; 13

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

20

```

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20                      25                      30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35                      40                      45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50                      55                      60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65                      70                      75                      80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85                      90                      95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100                      105                      110

ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct 384
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
      115                      120                      125

gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac 432
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
      130                      135                      140

tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc 480
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
      145                      150                      155                      160

tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct 528
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
      165                      170                      175

acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 564
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      180                      185

```

&lt;210&gt; 14

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

21

&lt;400&gt; 14

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 115 120 125

Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 130 135 140

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
 145 150 155 160

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 165 170 175

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

&lt;210&gt; 15

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion  
 between murine OPGL, residues 158-316 with tetanus  
 toxoid P2 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(546)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(336)  
 <223> Murine OPGL, residues 158-255

<220>  
 <221> misc\_feature  
 <222> (382)..(546)  
 <223> Murine OPGL, residues 262-316

<220>  
 <221> misc\_feature  
 <222> (337)..(381)  
 <223> Tetanus toxoid P2 epitope

<400> 15  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met  
 100 105 110  
 cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn  
 115 120 125

23

tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt 432  
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 130 135 140  
  
 ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac 480  
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 145 150 155 160  
  
 cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc 528  
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 165 170 175  
  
 aaa gtt cag gac atc gac 546  
 Lys Val Gln Asp Ile Asp  
 180

&lt;210&gt; 16

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion  
 between murine OPGL, residues 158-316 with tetanus  
 toxoid P2 epitope introduced, and His tag

&lt;400&gt; 16

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
  
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met  
 100 105 110  
  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn  
 115 120 125  
  
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 130 135 140

24

Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 145 150 155 160

Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 165 170 175

Lys Val Gln Asp Ile Asp  
 180

&lt;210&gt; 17

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P2 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(432)

&lt;223&gt; Murine OPGL, residues 158-287

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (478)..(519)

&lt;223&gt; Murine OPGL, residues 303-316

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (433)..(477)

&lt;223&gt; Tetanus toxoid P2 epitope

&lt;400&gt; 17

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30



25

```

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35              40              45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50              55              60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65              70              75              80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85              90              95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
      130              135              140

cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg gac 480
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
      145              150              155              160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      165              170

<210> 18
<211> 173
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Fusion between
      murine OPGL, residues 158-316 with tetanus toxoid
      P2 epitope introduced, and His tag

<400> 18
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1              5              10              15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20              25              30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly

```

26

35	40	45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val		
50	55	60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His		
65	70	75 80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val		
	85	90 95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met		
	100	105 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe		
	115	120 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu		
	130	135 140
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp		
	145	150 155 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		
	165	170

&lt;210&gt; 19

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion between  
murine OPGL, residues 158-316 with tetanus toxoid  
P30 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(231)

&lt;223&gt; Murine OPGL, residues 158-220

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (295)..(519)

&lt;223&gt; Murine OPGL, residues 242-316

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (232)..(294)

&lt;223&gt; Tetanus toxoid P30 epitope

&lt;400&gt; 19

```

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
   1                   5                   10                   15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tgc atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
                   20                   25                   30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
                   35                   40                   45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
   50                   55                   60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
   65                   70                   75                   80

ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac 288
Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
                   85                   90                   95

ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
                   100                   105                   110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
                   115                   120                   125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
                   130                   135                   140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
                   145                   150                   155                   160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                   165                   170

```

&lt;210&gt; 20

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion between  
murine OPGL, residues 158-316 with tetanus toxoid  
P30 epitope introduced, and His tag

&lt;400&gt; 20

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn  
65 70 75 80

Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His  
85 90 95

Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
165 170

&lt;210&gt; 21

&lt;211&gt; 68

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 21  
 agctgcagggt agtcggttgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60  
 gcgtacag 68

<210> 22  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR  
 primer

<400> 22  
 ctcacatctgac catcaacgct gcat 24

<210> 23  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR  
 primer

<400> 23  
 tttcgggtacc ctcagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60  
 gtag 64

<210> 24  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR  
 primer

<400> 24  
 tgagggtacc gaaagtttct gcttctcacc tggaaggttaa aaccctatc aaaatccaat 60  
 c 61

<210> 25  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR

## primer

<400> 25  
tttcggtacc ctcagccaga aagaaacggt gaagttggtg aacatcaggt tatgtgaaga 60  
ttg 63

<210> 26  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 26  
tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60  
at 62

<210> 27  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 27  
tacctgcagc tgatggttta cgttggttaa acccctatca aaatccaatc ttcacataac 60  
ctgatgcagt acatcaaag 79

<210> 28  
<211> 83  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 28  
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60  
ttgatgtact gcatcagggt atg 83

<210> 29  
<211> 49  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

&lt;400&gt; 29

gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg

49

&lt;210&gt; 30

&lt;211&gt; 53

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

&lt;400&gt; 30

gctaattcga aattcatcgg tatcaccgaa ctggacgcta cctacttcgg ggc

53

&lt;210&gt; 31

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

&lt;400&gt; 31

cttactagtc gatgtcctga actttg

26

&lt;210&gt; 32

&lt;211&gt; 74

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

&lt;400&gt; 32

agtgaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60  
aagatgggat ttg 74

&lt;210&gt; 33

&lt;211&gt; 65

&lt;212&gt; DNA

&lt;213&gt; Clostridium tetani

&lt;400&gt; 33

actacctgca gctgatgggt tacgttggtta aaacctctat caaaatccca tcttcacata 60  
 acctg 65

&lt;210&gt; 34

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Clostridium tetani

&lt;400&gt; 34

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
 1 5 10 15

&lt;210&gt; 35

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Clostridium tetani

&lt;400&gt; 35

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 1 5 10 15

Ala Ser His Leu Glu

20